

(FILE 'HOME' ENTERED AT 13:42:21 ON 18 JAN 2005)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 13:42:24 ON 18 JAN 2005

```
L1      241862 S ACETYLTRANSFERASE OR TRANSFERASE
L2      93 S L1 (2N) (INACTIVATING)
L3      5 S L2 (3N) STREPTOGRAMIN
L4      3 DUP REM L3 (2 DUPLICATES REMOVED)
L5      101 S VATE
L6      24 S L5 AND STREPTOGRAMIN
L7      16 DUP REM L6 (8 DUPLICATES REMOVED)
L8      0 S L7 AND TRANSFERASE
L9      4 S L7 AND L1
```

FILE 'STNGUIDE' ENTERED AT 13:46:08 ON 18 JAN 2005

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 13:46:59 ON 18 JAN 2005

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L10     16444 S SATG
L11     122 S L10 AND L1
L12     11 S L11 AND STREPTOGRAMIN
L13     7 DUP REM L12 (4 DUPLICATES REMOVED)
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=>

L13 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2005 ACS on STN  
 AN 1999:434756 CAPLUS  
 DN 131:195157  
 TI Characterization of a new enterococcal gene, **satG**, encoding a putative **acetyltransferase** conferring resistance to **streptogramin A** compounds  
 AU Werner, G.; Witte, W.  
 CS Robert Koch Institute Wernigerode Branch, Wernigerode, D-38855, Germany  
 SO Antimicrobial Agents and Chemotherapy (1999), 43(7), 1813-1814  
 CODEN: AMACQ; ISSN: 0066-4804  
 PB American Society for Microbiology  
 DT Journal  
 LA English  
 AB A quinupristin-dalfopristin-resistant *Enterococcus faecium* was isolated from a sewage treatment plant in Germany. PCR primers, based on conserved motifs in the *vat*, *satA* and *vatB* genes, were prepared and found to produce 144-147-bp fragments from these 3 genes. Use of these primers with the antibiotic-resistant *E. faecium* produced a 150-bp fragment. This fragment was used as a probe to identify and clone the corresponding gene, called **satG**. There was significant homol. between the amino acid sequence of the encoded protein and **streptogramin acetyltransferases**. Based on the **satG** sequence, two primers specific for the **satG** gene were prepared Preliminary results of a search for **streptogramin**-resistant enterococci revealed the existence of the **satG** gene in 9 or 23 isolated from sewage, 6 of 24 isolated from broiler samples, and all 17 isolates from poultry manure. Of 62 quinupristin-dalfopristin-resistant *E. faecium* isolates from hospitals in Germany, 9 were pos. for **satG**. The high number of **satG** isolates from poultry meat and manure may be due to selection of these bacteria by use of virginiamycin as a feed additive, and spread of the resistance via the food chain to humans is very likely. This hypothesis is being investigated.  
 RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD

*(b)(4) fully declaration filed.*

L9 ANSWER 2 OF 4 MEDLINE on STN  
 AN 2000493820 MEDLINE  
 DN PubMed ID: 10868806  
 TI Quinupristin/dalfopristin-resistant enterococci of the satA (vatD) and satG (vatE) genotypes from different ecological origins in Germany.  
 AU Werner G; Klare I; Heier H; Hinz K H; Bohme G; Wendt M; Witte W  
 CS Robert Koch Institute, Wernigerode Branch, Germany.. wernerg@rki.de  
 SO Microbial drug resistance (Larchmont, N.Y.), (2000 Spring) 6 (1) 37-47.  
 Journal code: 9508567. ISSN: 1076-6294.  
 CY United States  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 200010  
 ED Entered STN: 20001027  
 Last Updated on STN: 20001027  
 Entered Medline: 20001013  
 AB The semisynthetic **streptogramin** combination quinupristin/dalfopristin (Synercid) is a promising alternative for treatment of infections due to multiply resistant gram-positive bacteria including vancomycin-resistant Enterococcus faecium. Resistance is mediated by **acetyltransferases** SatA (VatD) or SatG (VatE). Recent papers have indicated a possible link between the use of the **streptogramin** virginiamycin S/M as a feed additive in commercial animal husbandry and a selection of quinupristin/dalfopristin-resistant E. faecium (QDRE). We screened manure samples from two different turkey farms and from six different pig farms (using virginiamycin), samples from a sewage water treatment plant, 24 broiler carcasses, 10 pork samples, and 200 stool samples of nonhospitalized humans for QDRE. Our strain culture collection of hospital E. faecium isolates from the last 2 years was also reviewed for QDRE. All manure and sewage samples were positive for QDRE, as well as 11 from broiler carcasses (46%), 1 from pork (10%), and 28 from human stool specimens (14%). Thirty-six hospital isolates of E. faecium exhibited resistance to quinupristin/dalfopristin. In 141 QDRE of different origin satA (vatD) and satG (vatE) genes were detected (seven isolates from humans with an unknown resistance mechanism). **Streptogramin** resistance determinants were transferable in filtermating experiments for 5 of 10 satA (vatD) and 9 of 22 satG (vatE) isolates. Different EcoRI patterns of satG (vatE) plasmids and corresponding hybridizations of the satG (vatE) gene indicated nonhomologous resistance plasmids in isolates of different origin. The results of this study indicate a common gene pool for **streptogramin** resistance in E. faecium of different ecological origin. A selection of QDRE using the **streptogramin** virginiamycin S/M as a feed additive and a spread of the resistance via the food chain to humans is probable.

*auth. bad date.*

RESULT 1

US-09-446-301A-10

; Sequence 10, Application US/09446301A

; Patent No. 6506893

; GENERAL INFORMATION:

; APPLICANT: EL SOLH, NEVINE

; APPLICANT: ALLIGNET, JEANINE

; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE

; TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED

; TITLE OF INVENTION: COMPOUNDS

; FILE REFERENCE: 03715-0059

; CURRENT APPLICATION NUMBER: US/09/446,301A

; CURRENT FILING DATE: 1999-12-20

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Staphylococcus sp.

US-09-446-301A-10

Query Match 100.0%; Score 33; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNDVW 5

|||||

Db 1 GNDVW 5

RESULT 1

US-09-446-301A-9

; Sequence 9, Application US/09446301A

; Patent No. 6506893

; GENERAL INFORMATION:

; APPLICANT: EL SOLH, NEVINE

; APPLICANT: ALLIGNET, JEANINE

; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE

; TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED

; TITLE OF INVENTION: COMPOUNDS

; FILE REFERENCE: 03715-0059

; CURRENT APPLICATION NUMBER: US/09/446,301A

; CURRENT FILING DATE: 1999-12-20

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Staphylococcus sp.

US-09-446-301A-9

Query Match 100.0%; Score 39; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IMNGANH 7

|||||||

Db 1 IMNGANH 7

RESULT 2

US-09-099-932-14/c

; Sequence 14, Application US/09099932

; Patent No. 6570001

; GENERAL INFORMATION:

; APPLICANT: El Solh, Nevine

; APPLICANT: Allignet, Jeanine

; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE

; TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED

; TITLE OF INVENTION: COMPOUNDS

; FILE REFERENCE: 03495.0173-00000

; CURRENT APPLICATION NUMBER: US/09/099,932

; CURRENT FILING DATE: 1998-06-19

; EARLIER APPLICATION NUMBER: 60/050,380

; EARLIER FILING DATE: 1997-06-20

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Staphylococcus

US-09-099-932-14

Query Match 81.3%; Score 12.2; DB 4; Length 21;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCANACRTCRTTNCC 15

||| ||:||||| ||

Db 15 CCAHACATCRTTYCC 1

RESULT 1  
 AV113293/c  
 LOCUS AV113293 260 bp mRNA linear EST 29-JUN-1999  
 DEFINITION AV113293 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA  
 clone 2610020H16, mRNA sequence.  
 ACCESSION AV113293  
 VERSION AV113293.1 GI:5267373  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 260)

AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,  
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,  
 Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,  
 Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H.,  
 Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,  
 Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y.,  
 Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,  
 Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs

JOURNAL Unpublished (1999)

COMMENT Contact: Chie Owa  
 Genome Science Laboratory  
 RIKEN  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-9145  
 Fax: 81-298-36-9098  
 Email: genome-res@rtc.riken.go.jp  
 Thermostabilization and thermoactivation of thermolabile enzymes by  
 trehalose and its application for the synthesis of full length cDNA  
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
 Transcriptional sequencing: A method for DNA sequencing using RNA  
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
 further details.

FEATURES Location/Qualifiers  
 source 1. .260  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="2610020H16"  
 /sex="mixed"  
 /dev\_stage="10-day embryo"  
 /clone\_lib="Mus musculus C57BL/6J 10-day embryo"

ORIGIN

Query Match 83.3%; Score 15; DB 9; Length 260;  
 Best Local Similarity 72.2%; Pred. No. 3.1e+03;  
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATHATGAAYGCNAAAYCAY 18  
 ||:|||||:| | |:|:  
 Db 27 ATCATGAATGCCAATCAT 10

Database :       Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
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- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
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- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
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- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
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1	227	35.4	630	13	US-10-282-122A-10335	Sequence 10335, A
2	212.2	33.1	624	13	US-10-282-122A-31033	Sequence 31033, A
3	195.2	30.4	636	15	US-10-253-904-2	Sequence 2, Appli
4	195.2	30.4	636	15	US-10-392-970-2	Sequence 2, Appli
5	195.2	30.4	1607	15	US-10-253-904-16	Sequence 16, Appl
6	195.2	30.4	1607	15	US-10-392-970-50	Sequence 50, Appl
7	178.4	27.8	660	9	US-09-452-599-175	Sequence 175, App
8	178.4	27.8	660	15	US-10-121-120-175	Sequence 175, App



Database : Issued\_Patents\_NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	195.2	30.4	636	4	US-09-446-301A-2	Sequence 2, Appli	
2	195.2	30.4	636	4	US-09-099-932-2	Sequence 2, Appli	
3	195.2	30.4	1607	4	US-09-446-301A-16	Sequence 16, Appl	
4	195.2	30.4	1607	4	US-09-099-932-50	Sequence 50, Appl	
5	178.4	27.8	660	2	US-08-743-637B-175	Sequence 175, App	
6	178.4	27.8	660	3	US-08-526-840B-175	Sequence 175, App	
7	162.6	25.3	630	2	US-08-743-637B-173	Sequence 173, App	
8	162.6	25.3	630	3	US-08-526-840B-173	Sequence 173, App	
9	79.2	12.3	657	4	US-09-543-681A-112	Sequence 112, App	
10	69	10.7	651	4	US-09-134-000C-2838	Sequence 2838, Ap	
11	68.6	10.7	636	4	US-09-328-352-1349	Sequence 1349, Ap	
12	67.8	10.6	11474	4	US-09-495-406-1	Sequence 1, Appli	
c 13	63.4	9.9	831	4	US-09-252-991A-13229	Sequence 13229, A	

Database : N\_Geneseq\_29Jan04:\*  
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 2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
 5: geneseqn2001bs:\*  
 6: geneseqn2002s:\*  
 7: geneseqn2003as:\*  
 8: geneseqn2003bs:\*  
 9: geneseqn2003cs:\*  
 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		% Query						
Result No.	Score	Match	Length	DB	ID	Description		
1	642	100.0	1080	4	AAF56835	Aaf56835	E. faeciu	
2	639.4	99.6	840	4	AAF56844	Aaf56844	E. faeciu	
3	637.2	99.3	645	4	AAH01592	Aah01592	Enterococ	
4	230.4	35.9	639	4	AAH01620	Aah01620	Staphyloc	
5	227	35.4	630	7	ACA22465	Aca22465	Prokaryot	
6	212.2	33.1	624	7	ACA43163	Aca43163	Prokaryot	
7	195.2	30.4	636	2	AAX09026	Aax09026	VatC stre	
8	195.2	30.4	639	4	AAH01625	Aah01625	Staphyloc	
9	178.4	27.8	660	2	AAT28572	Aat28572	Bacterial	
10	178.4	27.8	660	4	ABA76999	Aba76999	Antibioti	
11	162.6	25.3	630	2	AAT28570	Aat28570	Bacterial	
12	162.6	25.3	630	4	ABA76997	Aba76997	Antibioti	
13	155	24.1	611	7	ACA22140	Aca22140	Prokaryot	

36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%					Description
	No.	Score	Match Length	DB	ID	
	1	642	100.0	642	6	AX081253 Sequence
	2	642	100.0	1080	1	AF153312 Enterococ
	3	639.4	99.6	840	6	AX081266 Sequence
	4	637.2	99.3	645	6	AX110852 Sequence
	5	637.2	99.3	904	1	AF139725 Enterococ
	6	637.2	99.3	5522	1	AF229200 Enterococ
	7	637.2	99.3	7543	1	AF242872 Enterococ
c	8	637.2	99.3	19389	1	LFE488494 Lactobaci
	9	635.6	99.0	645	1	AY043212 Enterococ
	10	634	98.8	645	1	AY043209 Enterococ
	11	634	98.8	645	1	AY043211 Enterococ
	12	632.4	98.5	645	1	AY043210 Enterococ
	13	619.6	96.5	645	1	AY043213 Enterococ
	14	616.6	96.0	5535	1	AF406971 Enterococ
	15	605.2	94.3	645	1	AY008284 Enterococ
	16	230.4	35.9	639	6	AX110880 Sequence
	17	230.4	35.9	800	1	SAU19459 Staphylococ
	18	227	35.4	290685	1	AE017032 Bacillus
	19	224.6	35.0	300893	1	AE017006 Bacillus
	20	212.2	33.1	11080	1	AE006160 Pasteurel

Database : SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1139	100.0	214	2	Q9RG57	Q9rg57 enterococcu
2	1127	98.9	214	2	Q9XCL3	Q9xcl3 enterococcu
3	1127	98.9	214	2	Q84EW5	Q84ew5 lactobacill
4	1121	98.4	214	2	Q939C2	Q939c2 enterococcu
5	1119	98.2	214	2	Q939B9	Q939b9 enterococcu
6	1116	98.0	214	2	Q939C0	Q939c0 enterococcu
7	1115	97.9	214	2	Q939C1	Q939c1 enterococcu
8	1110	97.5	214	2	Q9ALL7	Q9all7 enterococcu
9	1095	96.1	214	2	Q939B8	Q939b8 enterococcu
10	1094	96.0	207	2	Q93CL9	Q93cl9 enterococcu
11	687	60.3	212	2	Q57156	Q57156 staphylococ

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	552.5	48.5	209	1	SATA_ENTFC	P50870 enterococcu
2	542	47.6	219	1	VATA_STAAU	P26839 staphylococ
3	515	45.2	180	1	MATA_BACSH	P26840 bacillus sp
4	359.5	31.6	210	1	CAT4_ENTAE	P50868 enterobacte
5	359	31.5	209	1	CAT4_AGRT5	P23364 agrobacteri
6	355.5	31.2	210	1	CAT4_MORMO	P50869 morganelle
7	347.5	30.5	210	1	CAT4_ECOLI	P26838 escherichia
8	328	28.8	212	1	CAT4_PSEAE	P26841 pseudomonas
9	177.5	15.6	214	1	YA64_METJA	Q58464 methanococc
10	161.5	14.2	172	1	CAPG_STAAU	P39856 staphylococ
11	159	14.0	203	1	THGA_ECOLI	P07464 escherichia
12	153.5	13.5	207	1	YA39_SCHPO	Q09707 schizosacch
13	152	13.3	184	1	MAA_BACSU	P37515 bacillus su
14	150.5	13.2	182	1	MAA_ECOLI	P77791 escherichia
15	144	12.6	196	1	WBBJ_ECOLI	P37750 escherichia
16	143.5	12.6	182	1	WCAF_ECOLI	P71240 escherichia
17	140	12.3	196	1	YJV8_YEAST	P40892 saccharomyc
18	135	11.9	183	1	NODL_RHIME	P28266 rhizobium m
19	131	11.5	159	1	Y304_METJA	Q57752 methanococc
20	129	11.3	262	1	LPXA_VIBVU	Q8dbe9 vibrio vuln
21	126.5	11.1	190	1	NODL_RHILV	P08632 rhizobium l

Database : PIR\_78:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	687	60.3	212	2	T10903	acetyltransferase
2	596.5	52.4	209	2	S75618	acetyltransferase
3	542	47.6	219	2	JN0822	acetyltransferase
4	495.5	43.5	210	2	F96995	acetyltransferase
5	417.5	36.7	218	2	AI2664	streptogramin A ac
6	417.5	36.7	218	2	H97446	attR protein (U594
7	413	36.3	259	2	AC3177	transacetylase [im
8	359	31.5	209	2	JN0132	chloramphenicol O-
9	359	31.5	209	2	AF3139	chloramphenicol ac
10	359	31.5	209	2	F98148	chloramphenicol ac
11	355.5	31.2	210	2	S49577	chloramphenicol O-
12	347.5	30.5	210	2	A41857	chloramphenicol O-
13	328.5	28.8	209	2	D82477	chloramphenicol ac
14	328	28.8	212	2	C83557	chloramphenicol ac

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	560	49.2	212	4	US-09-446-301A-5	Sequence 5, Appli
2	560	49.2	212	4	US-09-099-932-5	Sequence 5, Appli
3	560	49.2	507	4	US-09-446-301A-51	Sequence 51, Appl
4	327	28.7	277	4	US-09-252-991A-29304	Sequence 29304, A
5	268.5	23.6	218	4	US-09-543-681A-4284	Sequence 4284, Ap
6	254.5	22.3	211	4	US-09-328-352-5475	Sequence 5475, Ap
7	246.5	21.6	262	4	US-09-252-991A-22885	Sequence 22885, A
8	201	17.6	277	4	US-09-495-406-24	Sequence 24, Appl
9	165	14.5	204	4	US-09-328-352-6644	Sequence 6644, Ap
10	161	14.1	219	4	US-09-489-039A-12942	Sequence 12942, A
11	159.5	14.0	216	4	US-09-134-000C-6243	Sequence 6243, Ap
12	153	13.4	202	4	US-09-107-532A-4432	Sequence 4432, Ap
13	147.5	12.9	283	4	US-09-107-532A-6481	Sequence 6481, Ap
14	146.5	12.9	233	4	US-09-134-000C-6063	Sequence 6063, Ap